

Figure 1b

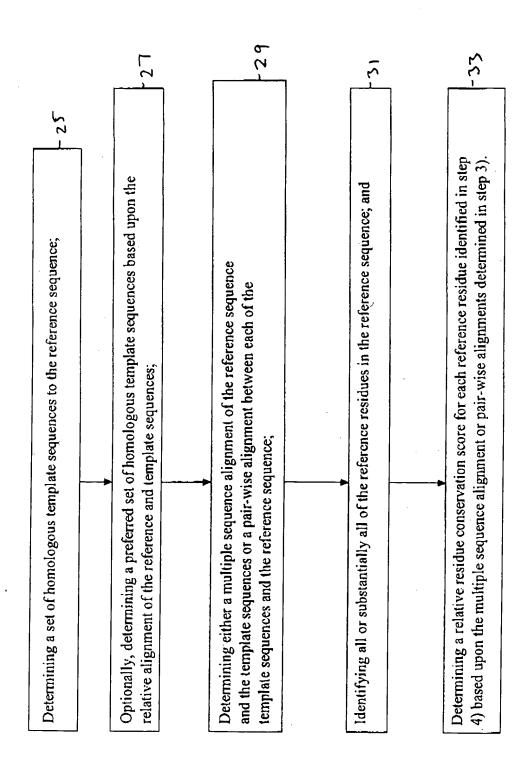
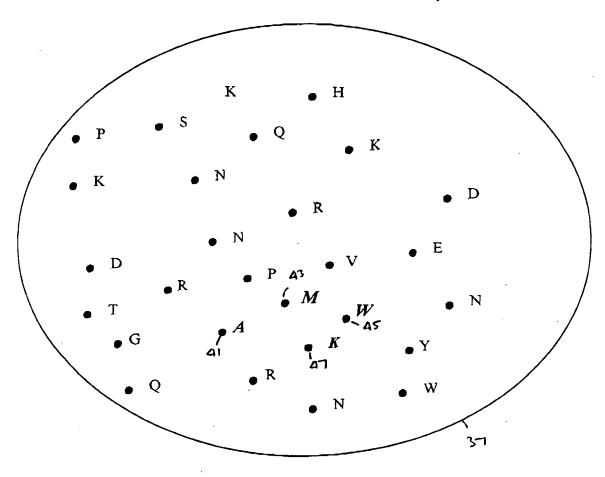


Figure 2



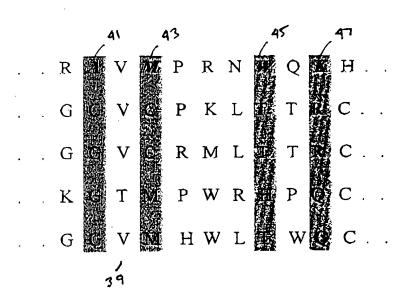
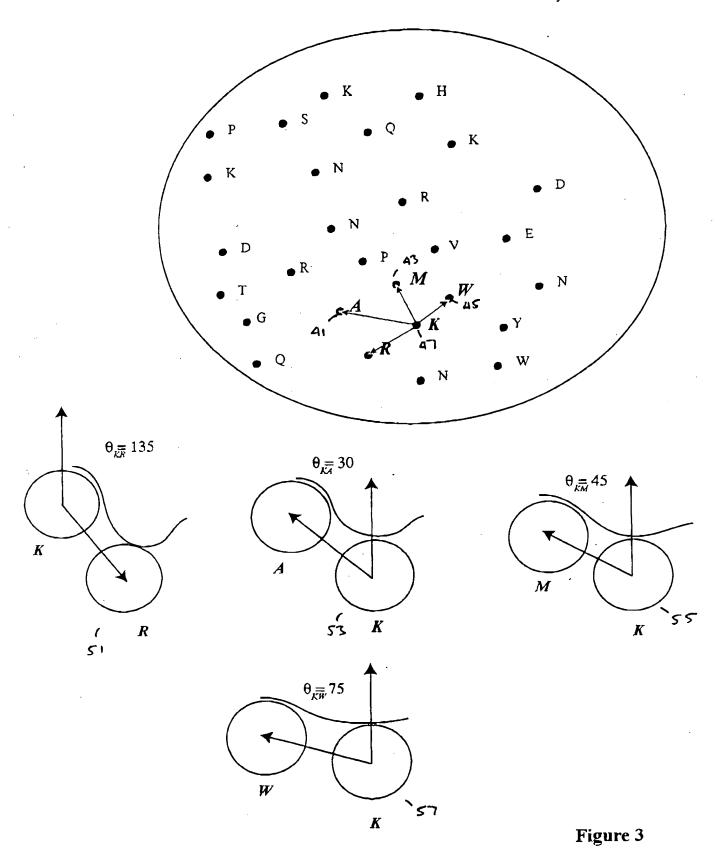
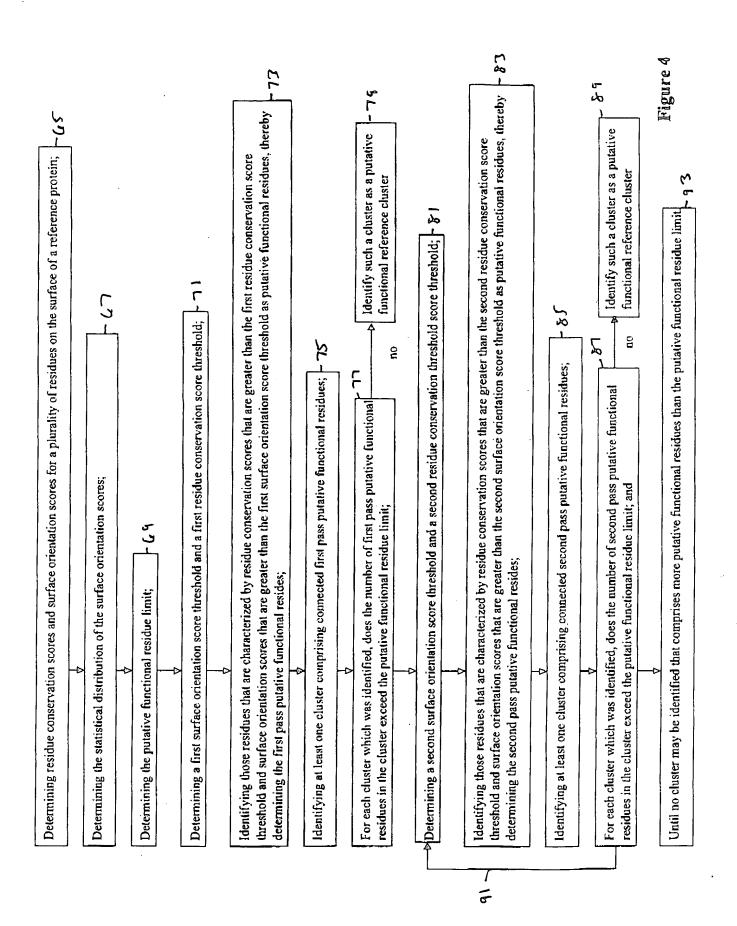
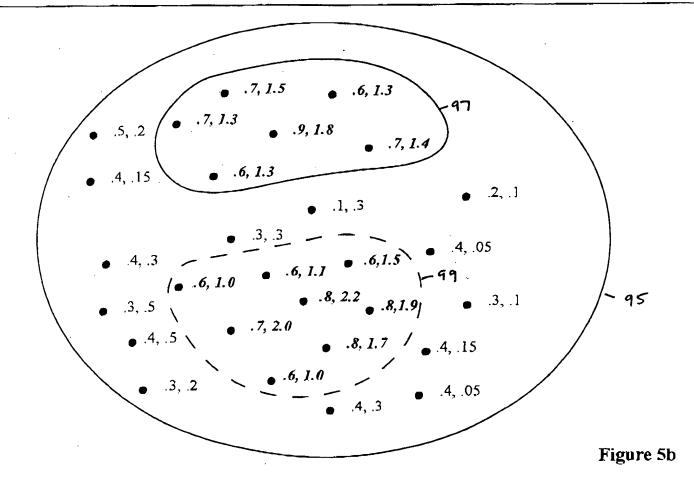


Figure 2b







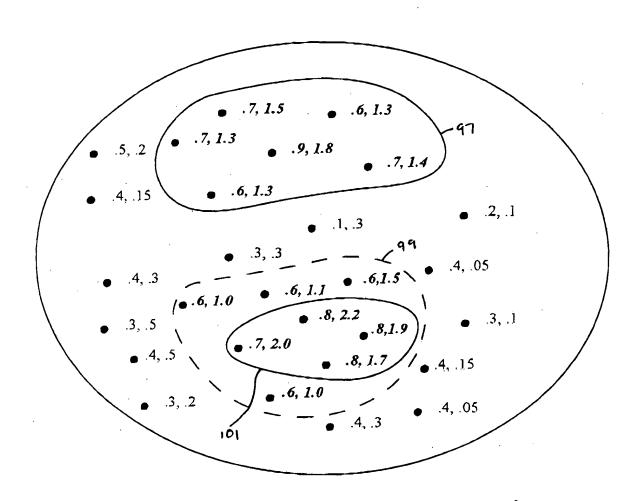


Figure 5c

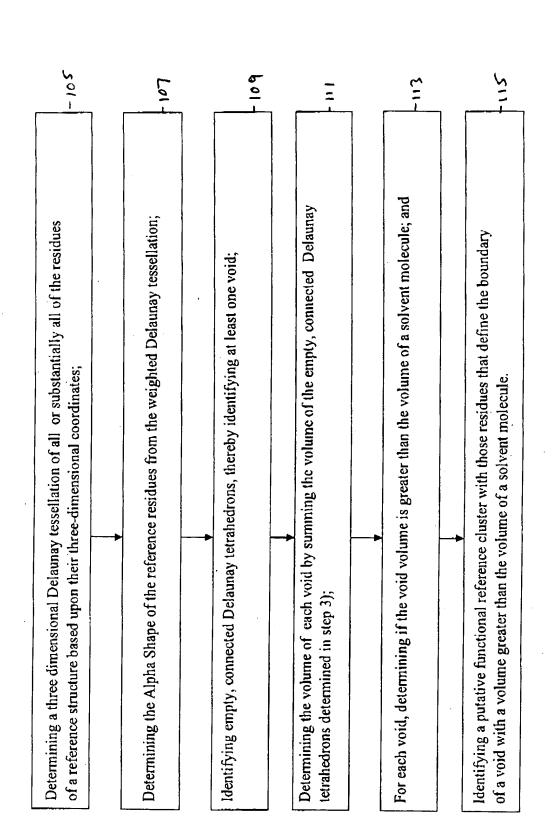
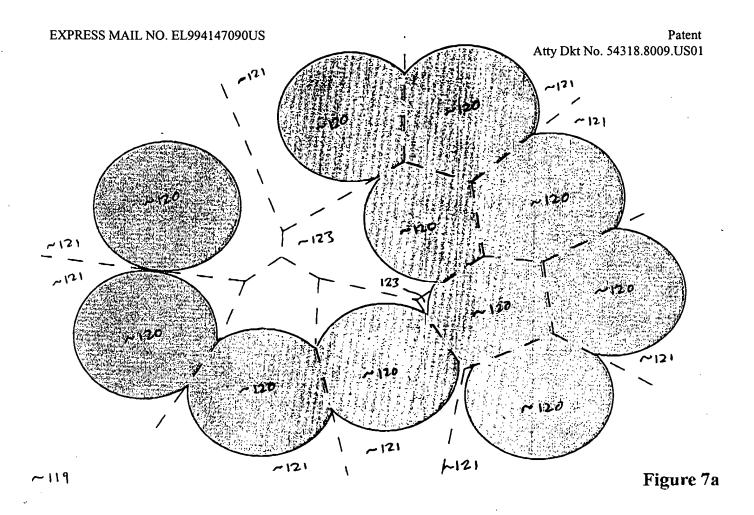
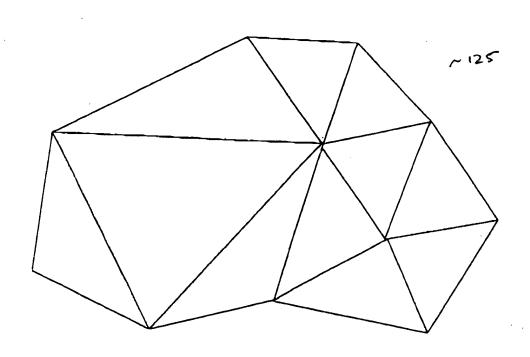


Figure (





PEST AND ADLE COPY Figure 7b

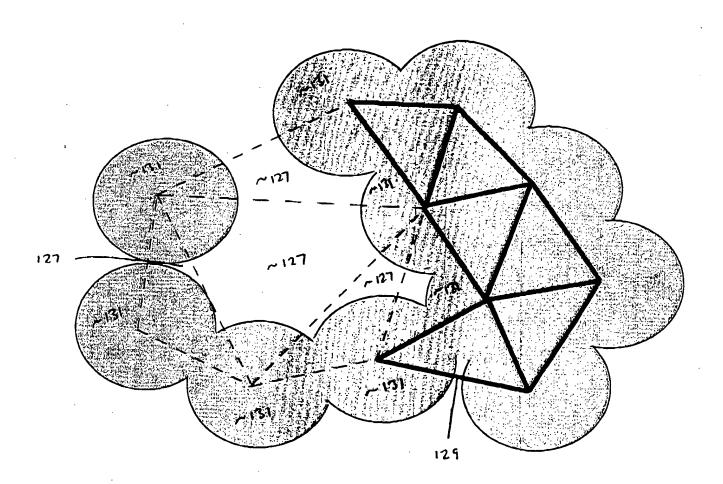


Figure 7c

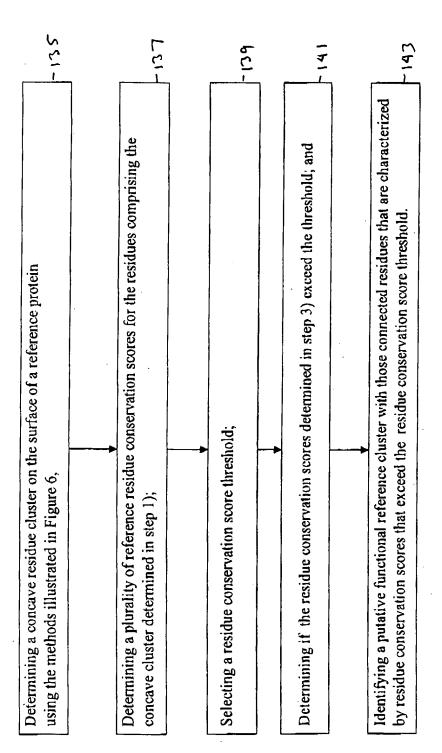


Figure 8

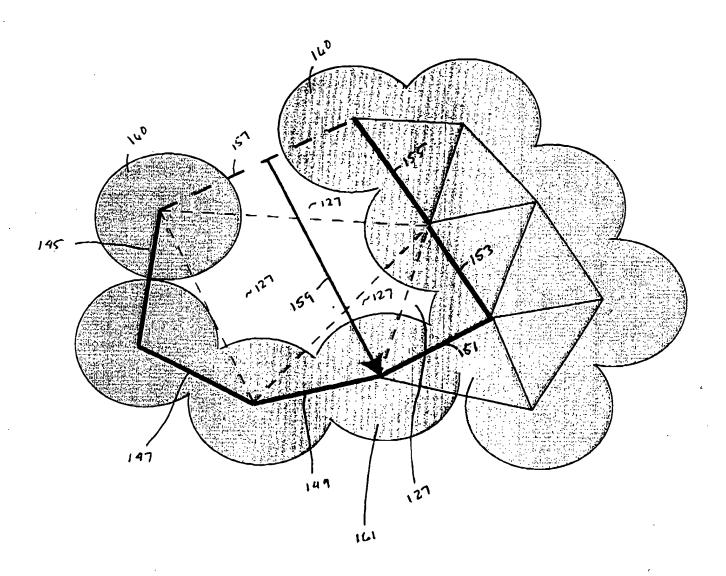
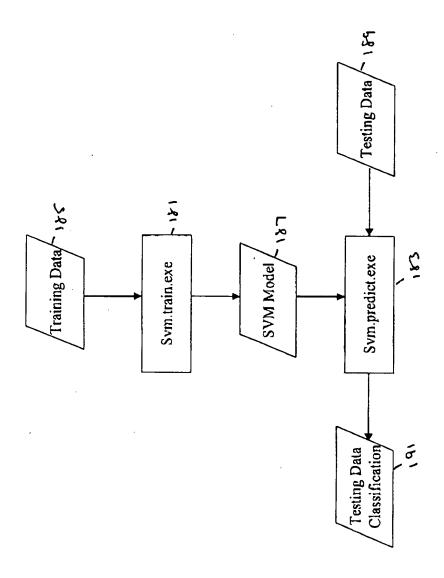


Figure 9



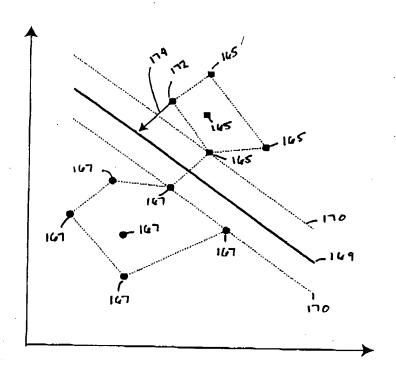


Figure 11

gi 21399686

Multiple Sequence Alignment of PDB:12asA Sequence with Template Sequences

gi	QUERY	AYIAKORQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVQVKVKALP
gi	24115047	AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGCEKAVQVKVKALP
gi	16762449	AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGCEKAVQVKVKALP
gi	16767161	AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGCEKAVQVKVKALP
gi	16120356	-FIQKQQQISFVKSFFSRQLEQQLGLIEVQAPILSRVGDGTQDNLSGSEKAVQVKVKSLP
gi	22536630	SFIHQQQEISFVKNTFTQYLIDKLEIVEVQGPILSQVGDGMQDNLSGIEHPVSVKVLNIP
gi	25010567	SFIHQQQEISFVKNTFTQYLIDKLEIVEVQGPILSQVGDGMQDNLSGIEHPVSVKVLNIP
gi	15901793	SFIHQQEEISFVKNTFTQYLKDKLEVVEVQGPILSKVGDGMQDNLSGVENPVSVKVLQIP
gi	15903827	SFIHQQEEISFVKNTFTQYLKDKLEVVEVQGPILSKVGDGMQDNLSGVENPVSVKVLOIP
gi	19746488	SFIHQQEEISFVKNTFTQYLIAKLDVVEVQGPILSRVGDGMQDNLSGTENPVSVNVLKIP
gi	15675438	SFIHQQEEISFVKNTFTQYLIAKLDVVEVQGPILSRVGDGMQDNLSGTENPVSVNVLKIP
g i.	16272507	TFILQQQEISFVKNTFTQNLIEQLGIIEVQGPILSQVGNGMQDNLSGIEKAVQVNVKCIP
gi	15603439	SFILQQQEISFAKNTFTEKLAEHLGIVEVQGPILSQVGNGIQDNLSGAEKAVQVNVKQIT
gi	23467425	SFILQQQEISFAKNTFTEKLIEHLGIIEVQGPILSQVGNGIQDNLSGTEKAVQVNVKQIT
gi	15639545	SFILQQQGISFAKHTFTQKLMEHLGLIEVQGPLLSQVGDGIQDGLSGREKAVSVSVKQIP
gi	30019890	QIAIKEVKTFFEDQLAKRLELFRVSAPLFVTKKSGLNDHLNGVERPIEFDMLHSG
gi	21399686	QIAIKEVKTFFEDQLAKRLELFRVSAPLFVTKKSGLNDHLNGVERPIEFDMLHSG
gi	28210498	AIKEVKDCFERALAKQLNLIRVSAPLFVRCDKGLNDNLNGVERPVKFTVKDDN
gi	23023030	
_	27887138	EIAIKKVKDFFESRLAKELDLLRVSAPLFVIPESGLNDNLNGTERPVSFDTKSGE
gi	19704111	EIAIKKVKDFFESHLSKELDLLRVSAPLFVIPESGLNDNLNGTERPVSFDTKSGE
gi	18310960	AIKELKDFFEDSLAKNLNLTRVSAPLFVNKGSGLNDDLNGIERPVSFDMKAMP
gi	23003194	AIVFIRETFQDKIAEKLNVQRMSAPMFVEKSTGLNDNLNGVERPVSFDMKAMP
	28377779	QQAIRYIRETFQDEFGKQLNL\$RL\$APMFVEKKTGLNDNLNGVEKPV\$FTMQDMG
gi	1703442	IAKRKRQSATSGKPSSEFGTAMNLERISAPMFVKKSSGLNDNLSGWEKPVSFTLHDGN
_	29347539	-LKQTELGIKQIKEFFQLNLSSELRLRRVTAPLFVLKGMGINDDLNGIERPVSFPIKDLG
_	26553601	SILETQKAIKFIKDLFQVNLAHALKLHRVTAPLVLERNKGINDDLNGSENPVTFTSDGNG
-	24762277	
gi	13357923	QKAIVEIKNSFQKHFAKNLNLSRVTAPLFVEGQSGLNDHLDHKQKAVSFYAKKLD
		•
a i l	OTTERV	DAGEGRAGIA PUNDOEL COMPEGA CHALLERAN LA DEPORT.
- :	QUERY 24115047	DAQFEVVHSLAKWKROTLGOHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVM
- !	16762449	DAQFEVVHSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVM
- :	16767161	DAQFEVVHSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVM
- !	16120356	DAQFEVVHSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVM
- :	22536630	DSTFEVVHSLAKWKRKTLGRFDFGADQGVYTHMKALRPDEDRLSAIHSVYVDQWDWERVM
- :	25010567	EAEFEVVHSLAKWKRHTLARFGFNEGEGLFVHMKALRPDEDSLDPTHSVYVDQWDWEKVI
- :	15901793	EAEFEVVHSLAKWKRHTLARFGFNEGEGLFVHMKALRPDEDSLDPTHSVYVDQWDWEKVI
- !	15903827	DATYEVVHSLAKWKRHTLARFGFGEGEGLFVHMKALRPDEDSLDATHSVYVDOWDWEKVI
- , ;	19746488	DATYEVVHSLAKWKRHTLARFGFGEGEGLFVHMKALRPDEDSLDATHSVYVDQWDWEKVI
	15675438	NATFEVVHSLAKWKRHTLARPGFNEGEGLVVNMKALRPDEDSLDQTHSVYVDQWDWEKVI
- :	16272507	NATFEVVHSLAKWKRHTLARFGFNEGEGLVVNMKALRPDEDSLDQTHSVYVDQWDWEKVI
	15603439	NAVFEVVHSLAKWKRHTLARFNFKEDEGLFVHMKALRPDEDSLDPTHSVYVDQWDWEKVI
- !	23467425	DATFEVVHSLAKWKRHTLARFNFAQGEGLFVHMTALRPDEDSLDQTHSVYVDOWDWEKVI
- ·	15639545	DAKFEVVHSLAKWKRHTLARFNFAENEGLFVHMKALRPDEDSLDQTHSVYVDQWDWEKVI
- !		GTAFEVVHSLAKWKRHTLARYGFQDNEGLFVHMIALRPDEDFLDQVRSVCVDQWDWEKVV
91	30019890	E-ELEIVHSLAKWKRFALHEYGYEAGEGLYTNMNAIRRDEE-LDATHSIYVDQWDWEKIV

Figure 12a

E-ELEIVHSLAKWKRFALHEYGYEAGEGLYTNMNAIRRDEE-LDATHSIYVDQWDWEKIV

	100010400	
-	28210498	EAAVEIVHSLAKWKRMALYRYNFNADEGLYTDMNAIRRDEE-LDNTHSIYVDQWDWERII
-	23023030	DMNAIRRDED-LDNLHSIYVDQWDWELVI
_	27887138	RVEIVHSLAKWKRMALYRYNIENHKGIYTDMNAIRRDED-TDFIHSYYVDQWDWEKII
_	19704111	RVEIVHSLAKWKRMALYRYNIENDKGIYTDMNAIRRDED-TDFIHSYYVDOWDWEKII
_	18310960	EFNIQIVHSLAKWKRLALHRYEFEHGEGLYTDMNAIRRDED-LDNIHSIYVDQWDWEKII
	23003194	NDTIEVVHSLAKWKRLALKRYGFGMHEGLYTNMNAIRRDED-LDNFHSIYVDQWDWEKII
_	28377779	DEQIEIVHSLAKWKRVALKRYGFDMHEGLYTNMNAIRKDED-LDNYHSAYVDQWDWEKVI
_	1703442	EGELQIVHSLAKWKRWALKHYGFSHGEGLFTNMNAIRKDEEVLDNLHSVYVDQWDWEKVI
_	29347539	DAQAEVVHSLAKWKRLTLADYNIEPGYGIYTDMNAIRSDEE-LGNLHSLYVDQWDWERVI
_	26553601	IS-GEIPQSLAKWKRMMLGKYEIPLHEGIYADMNAIRKDES-LSSIHSIYVDQWDWELHI
_	24762277	
gi	13357923	KT-LEIVQSLAKWKRLALLDYGFSLYEGLYTDMNAIRADDD-IDEIHSIYVDQWDWEILI
αi	QUERY	GDGERQFSTLKSTVEAIWAGIKATEAAVSEEFGLAPFLPDQIHFVHSQELLSRYPDLD
-	24115047	GDGERQLSTLKSTVEAIWAGIKATEAAVNEEFGLAPFLPDQIHFVHSQELLSRYPDLD
_	16762449	GDGERQFSTLKSTVEAIWAGIKATEAEVHKQFGLAPFLPDQIHFVHSQELLSRYPDLD
-	16767161	GDGERQFSILKSTVEAIWAGIKATEAEVHKQFGLAPFLPEQIQFVHSQELLARFPDLD
-	16120356	GDGERNLAYLKSTVNKIYAAIKETEAAISAEFGVKPFLPDHIQFIHSESLRARFPDLD
	22536630	PDGRRNLDYLKETVEKIYKAIRLTELAVEARFDIESILPKRITFIHTEELVEKYPDLS
	25010567	PDGRRNLDYLKETVEKIYKAIRLTELAVEARFDIESILPKRITFIHTEELVEKYPDLS
	15901793	
	15903827	PNGKRNIVYLKETVEKIYKAIRLTELAVEARYD IESILPKQITFIHTEELVERYPDLT PNGKRNIVYLKETVEKIYKAIRLTELAVEARYD IESILPKQITFIHTEELVERYPDLT
	19746488	PDGKRNLAYLKETVETIYKVIRLTELAVEARYDIEAVLPKKITFIHTEELVERYPDLT
_	15675436	PDGKRNLAYLKETVETIYKVIRLTELAVEARYDIEAVLPKKITFIHTEELVAKYPDLT
_	16272507	PEGRRNFAYLKETVNSIYRAIRLTELAVEARFDIPSILPKQITFVHSEDLVKRYPDLS
	15603439	
_	23467425	SAEQRNLAYLKETVRAIYAAILETEEAVSKKFGLATFLPKDIQFVHSEELVQRFPNMN
_	15639545	PTGRRNLAYLKETVRSIYQAILETEDAVHQKFGLSKFLPREITFIHSEELVQRYPELN
_	30019890	PVGSRNLAYLKDTVRKVYGALRESEVLVSERFGLRAFLPADIVFVQSEELVRRYPHLD
	21399686	QKEWRTVEYLQKTVQTIYGIFKDLEDHLFEKYPF-LGKYLPEEIVFVTSQELEDKYPELT
_	28210498	QKEWRTVDYLQKTVLTIYGIFKDLEDHLFEKYPF-LGKYLPEEIVFVTSQELEDKYPELT
_	23023030	KKEDRNEEYLKDIVRKIFKAFKETEEHINKLYPF-LGEVLPEEVFFMTTQELEDMFPDLT
	27887138	NKEDRNEETLKNIVKKIYNVLKKTEDFIAEQYPQ-IPKFLPEDIFFITTQELEDMYPELS
	19704111	SKEDRNEEYLKETVRKIYCVFKETEEYITTEYPK-LTKKLPEEITFITSQELENKYPNLT
	18310960	SKEDRNEEYLKDVVRKIYSVFKKTEEYITTEYPK-LTKKLPEEITFITAQELENKYPNLT
	23003194	DKEERNLETLKETVKSIYGTFKATEDFIVAKYPH-IEKILPEDITFITSQELEDRYPDLT
	28377779	SKDERNIDTLKDTVKQIFKAIKETEKEVAARYPS-STYRLPNEITFITTQELEDRWPDLT
- '	1703442	SKEERTVETLKAAVRQIFKVIKHMEHEVWYKFPQ-AVHHLPDEIHFLTTQELEDMYPDMT
- '	29347539	DKSERTEATLRQTVQRIFETIKGMEYHVRALYPQ-AAYHLPEEISFVTSEELEARWPSLT
	26553601	TNEDRNVEFLKEIVNRIYAAMIRTEYMVYEMYPO-IKPCLPQKLHFIHSEELRQLYPNLE
- :	24762277	KKTERNLETLKVVVKKIYEIIRLCQKEVNKKYEWFAENLLPEEITFISSEDLLQRYPNKT
- :	13357923	NNODONI DEI VOTINITTYONTONI TITANA DI ANALE DI CONTRA DI
9+1	1333/323	NNQDCNLDFLKSIVNKIYSTIRIVQLEIDQLYN-PKQIILPDSITFISSQELEDLYPHLS
gi	QUERY	AKGRERAIAKDLGAVFLVGIGGKLS-DGHRHDVRAPDYDDWSTPSELGHAGLNGDILVWN
:	24115047	AKGRERAIAKDLGAVFLVGIGGKLS-DGHRHDVRAPDYDDWSTPSELGHAGLNGDILVWN
	16762449	AKGRERAIAKELGAVFLVGIGGKLS-DGRRHDVRAPDYDDWSSASELGYAGLNGDILVWN
	16767161	AKGRERAIAKELGAVFLVGIGGKLS-DGHRHDVRAPDYDDWSSASELGYAGLNGDILVWN
- :	16120356	AKGRERAIAKELGAVFLIGIGGKLA-DGQSHDVRAPDYDDWTSPSAEGFSGLNGDIIVWN
	22536630	PKERENAIAKEYGAVFLIGIGGELA-DGKPHDGRAPDYDDWTTPSENGFKGLNGDILVWN

Figure 12b

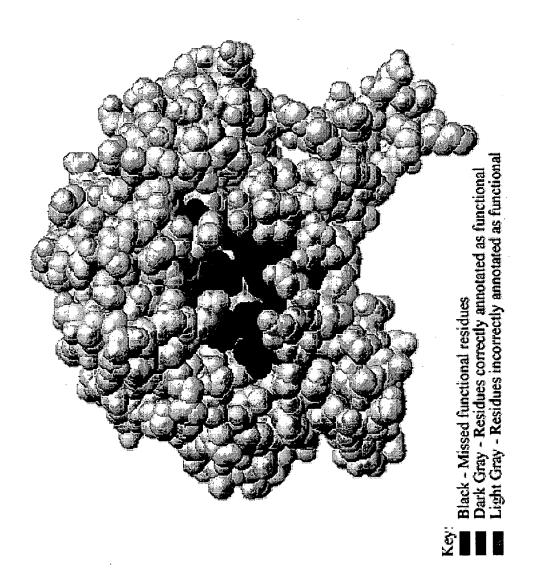
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g:	i 15901793	PKERENAICKEFGAVFLIGIGGELP-DGKPHDGRAPDYDDWTSESENGYKGLNGDILVWN
g:	i 15903827	SKERENAICKEFGAVFLIGIGGELP-DGKPHDGRAPDYDDWTSESENGYKGLNGDILVWN
	i 19746488	PKERENAITKEFGAVFLIGIGGVLP-DGKPHDGRAPDYDDWTTETENGYHGLNGDILVWN
g:	i 15675438	PKERENAITKEFGAVFLIGIGGVLP-DGKPHDGRAPDYDDWTTETENGYHGLNGDILVWN
g:	i 16272507	SKERENAICKEYGAVFLIGIGGKLS-DGKPHDGRAPDYDDWTTESENGYKGLNGDILVWN
gi	i 15603439	DKERENAICKEYGAVFLIGIGGKLS-DGKPHDVRAPDYDDWTTPSEGEYKGLNGDILVWN
gi	i 23467425	DKORENAICKEYGAVFLIGIGGVLS-DGKPHDKRAPDYDDWTTPSEGEYLGLNGDILVWN
gi	1 15639545	SKGREDAICKEHGAVFLIGIGGVLS-DGKPHDVRAPDYDDWTTPSEGEYKGLNGDILVWN
gi	1 30019890	PKDREHAIAKEHGAVFIIGIGDALR-SGEKHDGRAADYDDWKLNGDILFWH
gi	1 21399686	PKDREHAIAKEHGAVFIIGIGDALR-SGEKHDGRAADYDDWKLNGDILFWH
gi	28210498	AKEREDAITKEKKAVFLMKIGKTLE-SGEKHDGRAPDYDDWELNGDILFWN
gi	23023030	PKEREDAIAKEKKAIFLMKIGGVLK-SGKKHDGRAPDYDDWTLNGDIILWY
gi	. 27887138	PKNREHAAAKEYGAIFLMKIGGKLS-SGEKHDGRAPDYDDWDLNGDIIFNY
gi	. 19704111	PKNREHAAAKEYGAIFLMKIGGKLS-SGEKHDGRAPDYDDWDLNGDIIFNY
gi	18310960	SKERETAICKEFGAVFIIGIGGKLA-SGEKHDDRSPDYDDWTLNGDLLFYY
gi	23003194	PDEREDKIAKEKKAVFLMKIGDKLKRSGKPHDGRAPDYDDWQLNGDLLFWY
gi	28377779	PRERENAICKKLGCVFLMQIGWKLD-SGERHDGRAPDYDDWKLNGDILFWY
gi	1703442	PSEREDKI CQEKGAVFLEHIGGALPLSKKPHDLRAPDYDDWTLNGDLLFWY
gi	29347539	PKCREHAICQKYGAVFIIGIGCKLS-DGKKHDGRAPDYDDYTSTGLNNLPGLNGDLLLWD
gi	26553601	PKERERLIASKYKAVFIIGIGDNLS-DGKPHDLRAPDYDDWKLNGDIIVWN
-	24762277	PPTP*PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
gi	13357923	PSRREYEFAKIHKAIFIYQIGYPLK-SGYIQSIRSPEYDNWNLNGDLIVYH
		•
gi	QUERY	PVLEDAFELSSMGIRVDADTLKHQLALTGD-EDRLELEWHQALLRGEMPQTIGGGIGQSR
gi	24115047	PVLEDAFELSSMGIRVDADTLKHQLALTGD-EDRLOLEWHOALLRGEMPOTTGGGTGOSP
gi	16762449	PVLEDAFELSSMGIRVDADTLMRQLALTGD-EDRLQLEWHQALLRGEMPQTIGGGIGQSR
gi	16767161	PVLEDAFELSSMGIRVDADTLMRQLALTGD-EDRLQLEWHQALLRGEMPQTIGGGIGQSR
gi	16120356	PILEDAFEISSMGIRVDAEALKRQLALTGD-EDRLELEWHQSLLRGEMPQTIGGGIGQSR
gi	22536630	EQLGTAFELSSMGIRVDEDALKRQVVLTGD-EDRLEFEWHKTLLRGFFPLTIGGGIGOSR
gi	25010567	EQLGTAFELSSMGIRVDEDALKRQVVLTGD-EGRLEFEWHKTLLRGFFPLTIGGGIGQSR
gi	15901793	ESLGGAFELSSMGIRVDEETLRRQVEITGD-EDRLELEWHKSLLNGLFPLTIGGGIGOSR
	15903827	ESLGGAFELSSMGIRVDEETLRRQVEITGD-EDRLELEWHKSLLNGLFPLTIGGGIGQSR
gi	19746488	DQLGSAFELSSMGIRVDEEALKRQVEMTGD-QDRLAFDWHKSLLNGLFPLTIGGGIGQSR
gi	15675438	DQLGSAFELSSMGIRVDEEALKRQVEMTGD-QDRLGFDWHKSLLNGLFPLTIGGGIGQSR
gi	16272507	DQLGKAFELSSMGIRVDESALRLQVGLTGD-EDHLKMDWHQDLLNGKLPLTIGGGIGQSR
gi	15603439	PILERAFELSSMGIRVDETALRKQLALTNN-EDRLKFDWHQDLVNGRLPLSIGGGIGRSR
gi	23467425	PVLERAFEVSSMGIRVDETALRKQLALTGD-EDRLQFDWHQDLVNGRLPLSIGGGIGQSR
gi	15639545	PVLGRAFEVSSMGIRVDEGALRTQLALTGD-EDSLACSWHQDLINGRLPQSIGGGIGQSR
	30019890	PVLQSSFELSSMGIRVDSKSLDEQLTKTGE-DFKREYDFHKGILEDVLPLTTGGGTGOSP
gi	21399686	PVLQSSFELSSMGIRVDSKSLDEQLTKTGE-DFKREYDFHKGILEDVLPLTIGGGIGQSR
gi	28210498	PVLNKAFELSSMGIRVDEESLLKQLKLANC-EERKELQPHKMLLEKKLPYTIGGGIGQSR
gi	23023030	PLLERSFEISSMGIRVDENSLLSQ
gi	27867138	PLLGIGLELSSMGIRVDEKSLDEOLKIANC-EDRRSLPYHQMILNKVLPYTIGGGIGQSR
gi	19704111	PLLGIGLELSSMGIRVDEKSLDEQLKIANC-EDRRSLPYHQMILNKVLPYTIGGGIGQSR
gi	18310960	PLFDEAVELSSMGIRVDEESLLKQLKIAEC-EERKELPFHQMLLEGKLPYTIGGGIGQSR
gi	23003194	EPLORKLEISSMGIRVSEESLKTOLKKAHA-EERAALPFHKMLLNGELPYTIGGGIGOSR
gi	28377779	EPLDQAIEISSMGIRVDAESMKKQLKDVDA-EDRLSLPYHQMILNADVPYTIGGGIGQSR
		·

Figure 12c

gi 1703442	EPLQRAFEVSSMSIRVDEDRLQEQLKLAGA-EDRLDLPFHQALLKGDLPYSIGGGIGQSR
gi 29347539	DVLQRSIELSSMGVRVDREALQRQLKEENE-EERLKLYFHKRLMDDTLPLSIGGGIGQSR
gi 26553601	ETTKSALELSSMGIRVDEVSLVEQLDKSNN-NSRKELDFHKKLINKEFPYSIGGGIGOSR
gi 24762277	IRVNKEVLLKQLEESKQ-NERLELMFHKKLVNGELHQTIGGGIGQSR
gi 13357923	KLNDQAIELSSMGIRVSKQDFIKQTNFANLKNDQENNFYHQMILNNQLPQTIGGGIGQSR
91 (1333 / 323	VTVD Á YTDD 3 JAGTKA SVÁÐE TVÁ TAL YKDVAÐ Á FRAK TVÁ JITUM Á FIL FOLD Á TAL A TVÁ JAGT FARA Í TAGA TAGA TAGA T
gi QUERY	LTMLLLQLPHIGOVOAGVWPAAVRESVPSLL
gi 24115047	LTMLLLQLPHIGQVQCGVWPAAVRESVPSLL
gi 16762449	LTMLLLQLPHIGOVQCGVWPAOVRESIPAIL
gi 16767161	LTMLLLQLPHIGOVOCGVWPAOVRESIPAIL
gi 16120356	LVMLLLQKOHIGQVQCGVWGPEISEKVDGLL
gi 22536630	LAMFLLRKKHIGEVQSSVWPKEVRDTFENIL
gi 25010567	LAMFLLRKKHIGEVOSSVWPKEVRDTFENIL
gi 15901793	MAMFLLRKRHIGEVOTSVWPOEVRDTYENIL
gi 15903827	MAMFLLRKRHIGEVOTSVWPOEVRDTYENIL
gi 19746488	MVMFLLRKKHIGEVOTSVWPOEVRDSYDNIL
gi 15675438	MVMFLLRKQHIGEVQTSVWPQEVRDSYDNIL
gi 16272507	LAMLLLRKKHIGEVOSSVWPKEMLEEFSNIL
gi 15603439	LVMLLLQKKHIGEVOSSVWPKWVMEOFDNIL
gi 23467425	LAMLLLQKKHIGEVQSSVWPKVVTEQFENIL
gi 15639545	LAMLLLQRKHIGEVQASVWPRSVREEFENIL
gi 30019890	MCMYFLRKAHIGEVQSSVWPDDLREAC
gi 21399686	MCMYFLRKAHIGEVQSSVWPDDLREAC
gi 28210498	MCMLFLKKAHIGEVQSSIWPEEMIKFCEE
gi 23023030	
gi 27887138	ICMFFLDKLHIGEVQASIWSQEVHEIC
gi 19704111	ICMFFLDKLHIGEVQASIWSQEVHEIC
gi 18310960	ICMFFLRKAHIGEVQASMWDEDMIRTCEE
gi 23003194	LCMLLLGKAHIGEVQASIWPPKMIEECE
gi 28377779	LCMLLLGKAHVGEVQAALW
gi 1703442	LCMLLLQGPH-GEVQASIWPDEIVEKCQ
gi 29347539	LCMFYLRKAHIGEIQASIWPEDMRKECEEL-
gi 26553601	LCYFLLHKQHIGEVQSSLWPKDILEEAE
gi 24762277	LCYFLLQKDHIGEVQASHWSDEIVAE
gi 13357923	LCMFLLNKKHIGEVQVSVWPNEYKDEL
<i>-</i>	_

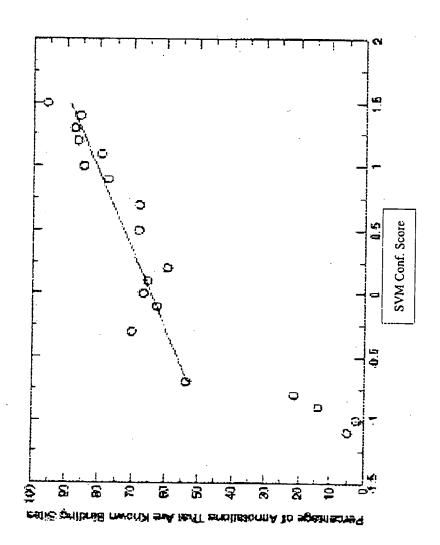
Figure 12d

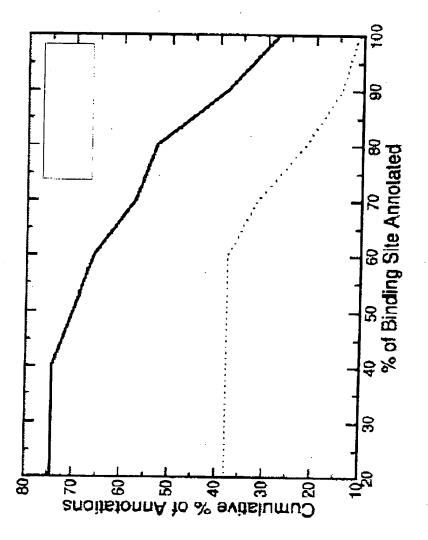
Figure 13



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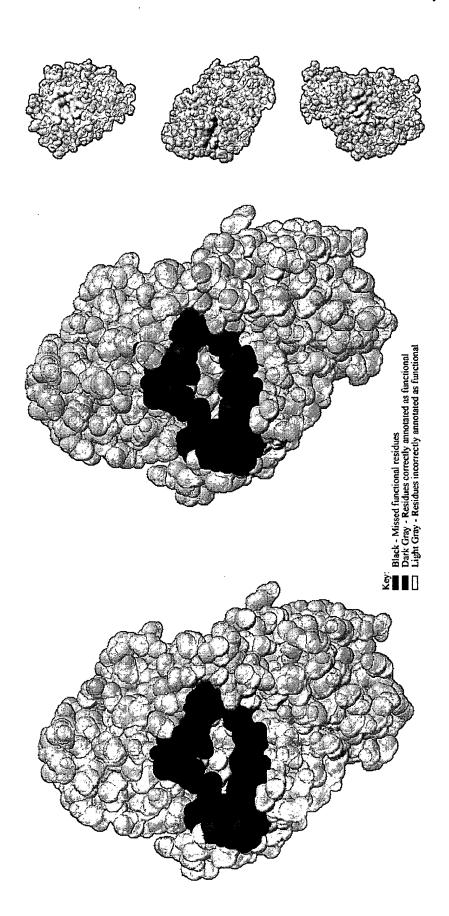
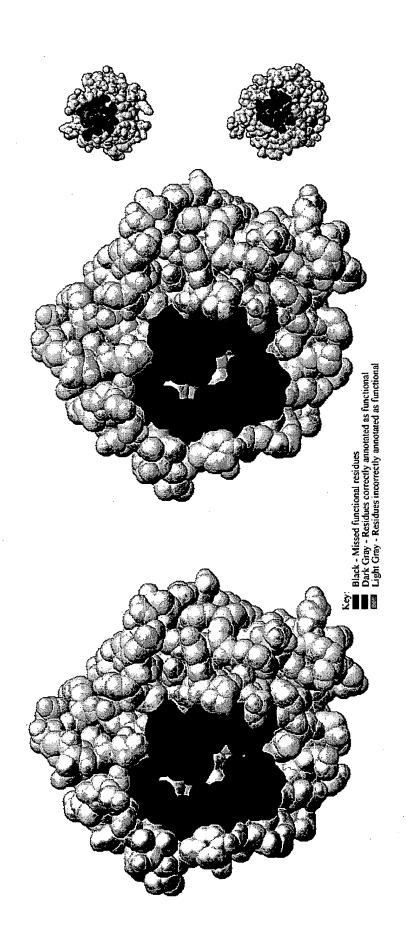
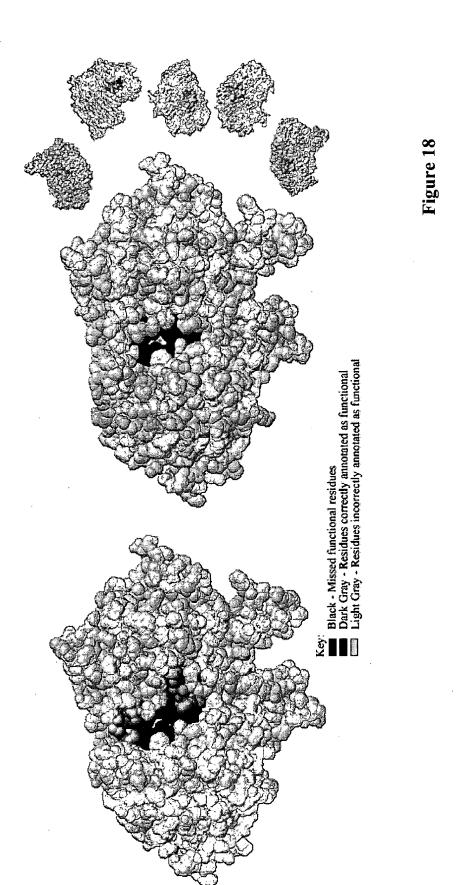
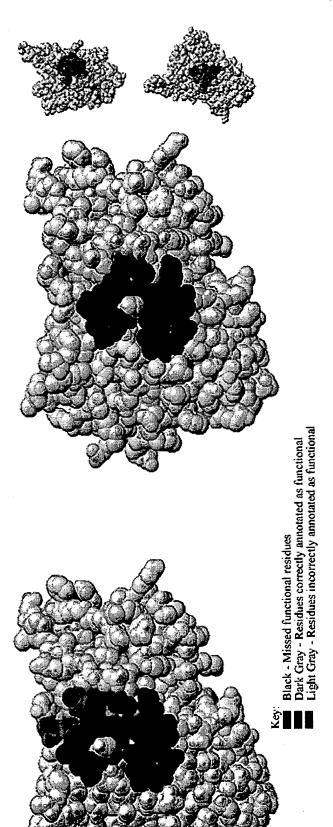


Figure 16

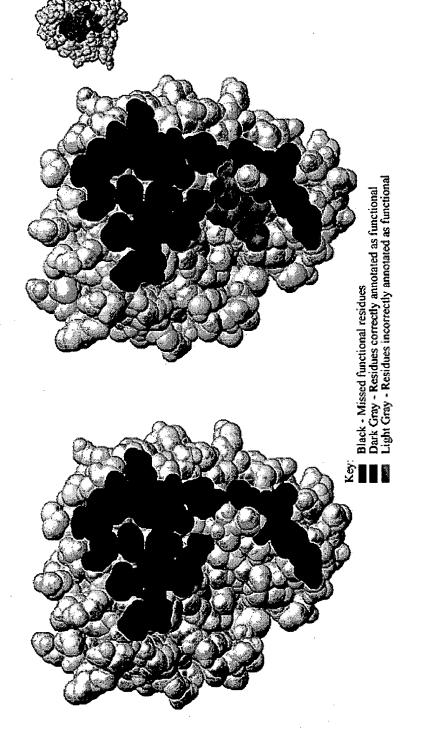




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Figure 21



